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1GCGA 4
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50
5 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 54
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100
55 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 104
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 150
105 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 154
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 200
155 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 204
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250
205 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 254
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300
255 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 304
301 GGATAGCTGGGTTCACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350
305 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 354
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400
355 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 404
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450
405 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 454
451 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 500
455 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 504
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
505 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 554
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
555 GATCAACGAAAACGCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 604
601 GATCAACGAAAACGCCGATTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 1A

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605 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 654
|||
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700

655 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 704
|||
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750

705 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 754
|||
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800

755 TGGCCAAAGATCGGATCACAGCCCTGTGATCAGTATCATGGCACGGCA 804
|||
801 TGGCCAAAGATCGGATCACAGCCCTGTGATCAGTATCATGGCACGGCA 850

805 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 854
|||
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900

855 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 904
|||
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950

905 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTATGGG 954
|||
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTATGGG 1000

955 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1004
|||
1001 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1050

1005 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1054
|||
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1100

1055 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1104
|||
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150

1105 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1154
|||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200

1155 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1204
|||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1250

1205 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1254
|||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig 1B

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1255 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1304
|||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350
|||||
1305 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1354
|||||
1351 GCGTTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400
|||||
1355 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCAC 1404
|||||
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCA 1447
|||||
1405 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1454
|||||
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497
|||||
1455 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1504
|||||
1498 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547
|||||
1505 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1554
|||||
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597
|||||
1555 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1604
|||||
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1647
|||||
1605 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1654
|||||
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697
|||||
1655 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1704
|||||
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747
|||||
1705 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1754
|||||
1748 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797
|||||
1755 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1804
|||||
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847
|||||
1805 AAAG..... 1808
|||||
1848 AAAGGCCCGAG 1858

Fig. 1C

Fig. 2A

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636 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 685
|||||
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700
686 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 735
|||||
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
736 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 785
|||||
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
786 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 835
|||||
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850
836 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 885
|||||
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
886 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCTGATCGGGCGGTAA 935
|||||
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCTGATCGGGCGGTAA 950
936 TGTGGACGCTTACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 985
|||||
951 TGTGGACGCTTACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000
986 ATGAGTCCCGCCGATTTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1035
|||||
1001 ATGAGTCCCGCCGATTTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1050
1036 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTGCGCTGCTGC 1085
|||||
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTGCGCTGCTGC 1100
1086 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1135
|||||
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150
1136 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1185
|||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200
1186 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1235
|||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1250
1236 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1285
|||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig. 2B

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1286 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1335
|||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350
|||||
1336 GCGTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1385
|||||
1351 GCGTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400
|||||
1386 GCGCGGACCTTATCCTGCTTGACCTGCGTCACCTCAGACGACTCCTCAC 1435
|||||
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCA 1447
|||||
1436 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1485
|||||
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497
|||||
1486 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1535
|||||
1498 CACTGTCCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547
|||||
1536 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1585
|||||
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597
|||||
1586 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1635
|||||
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1647
|||||
1636 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1685
|||||
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697
|||||
1686 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1735
|||||
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747
|||||
1736 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1785
|||||
1748 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797
|||||
1786 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1835
|||||
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847
|||||
1836 AAAGGCCCCGAG 1846
|||||
1848 AAAGGCCCCGAG 1858

Fig. 2C

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1ASMVTLTPLFSFSLNCTRKASRSVMSASSWLVT 35
1 SGNFLSAATAALIMKASMTLTPLF SFSLLNCTRKASRSVMSASSWLVT 50
36 GMTTQLRCRFFDGIISALRRVTHYWRHIMQTLSIQHGT LVTMDQYRRVLG 85
51 GMTTQLRCRFFDGIISALRRVTHYWRHIMQTLSIQHGT LVTMDQYRRVLG 100
86 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 135
101 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 150
136 LLRGGPSHGRQFYDWLFNVVYPGQKAMRPEDVAVAVRLYCAEAVRSGITT 185
151 LLRGGPSHGRQFYDWLFNVVYPGQKAMRPEDVAVAVRLYCAEAVRSGITT 200
186 INENADSAIYPGNIEAAMAVYGEVGVRRVYARMFFDRMDGRIQGYVDALK 235
201 INENADSAIYPGNIEAAMAVYGEVGVRRVYARMFFDRMDGRIQGYVDALK 250
236 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 285
251 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 300
286 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPAEMEYECYGLLDERL 335
301 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPAEMEYECYGLLDERL 350
336 QVAHCVYFDRKDVRLLRHNVKVASQVVS NAYLGSVAPVPEMVERGMAV 385
351 QVAHCVYFDRKDVRLLRHNVKVASQVVS NAYLGSVAPVPEMVERGMAV 400
386 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTP EKILEMATIDGA 435
401 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTP EKILEMATIDGA 450
436 RSLGMDHEIGSIETGKRADLILLDLRHLPQTTPHHHLAATIVFQAYGNEVD 485
451 RSLGMDHEIGSIETGKRADLILLDLRHLLRRLS.HHLAATIVFQAYGNEVD 499
486 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 535
500 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 549
536 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDDGYRIAMNAALPSFARVE 585
550 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDDGYRIAMNAALPSFARVE 599
586 SLVGEGRRLRAPASRRSE... 602
600 SLVGEGRRLRAPASRRGERPE 619

Fig. 3

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1  . . . . . SAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTG 45
   |||||||||||||||||||||||||||||||||||||||||||||||||||
1 SGNFLSAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTG 50

46 GMTTQLRCRFFDGVISALRRVTHYWRHIMQTLSIQHGTGLVTMDQYRRVLG 95
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
51 GMTTQLRCRFFDGVISALRRVTHYWRHIMQTLSIQHGTGLVTMDQYRRVLG 100
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
   . START .
96 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 145
   |||||||||||||||||||||||||||||||||||||||||||||||||||
101 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 150

146 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 195
   |||||||||||||||||||||||||||||||||||||||||||||||||||
151 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 200

196 INENADSAIYPGNIEAAMAVYGEVGVVRVYARMFFDRMDGRIQGYVDALK 245
   |||||||||||||||||||||||||||||||||||||||||||||||||||
201 INENADSAIYPGNIEAAMAVYGEVGVVRVYARMFFDRMDGRIQGYVDALK 250

246 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 295
   |||||||||||||||||||||||||||||||||||||||||||||||||||
251 ARSPQVELCSIMEETAVAKDRITALSDQYHGTAGGRISVWPAPATTTAVT 300

296 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 345
   ||||||||||||||||||||||||||||||||||||||||:|||||||||
301 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 350

346 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSQVAPVPEMVERGMAV 395
   |||||||||||||||||||||||||||||||||||||||||||||||||||
351 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSQVAPVPEMVERGMAV 400

396 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 445
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
401 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPEKILEMATIDGA 450

446 RSLGMDHEIGSIETGKRADLILLDLRHLPQTTPHHHLAATIVFQAYGNEVD 495
   |||||||||||||:|||||||||||||||||||||||||||||||||||||
451 RSLGMDHEIGSIETGKRADLILLDLRHLLRRLS.HHLAATIVFQAYGNEVD 499

496 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 545
   |||||||||||||||||||||||||||||||||||||||||||||||||||
500 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 549
   STOP
546 SIQEMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 595
   |||||||||||||||||||||||||||||||||||||||||||||||||||
550 SIQEMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 599

596 SLVGEGRRLRAPASRRSERPE 615
   |||||||||||||:|||||
600 SLVGEGRRLRAPASRRGERPE 619

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Fig. 4

Fig. 5A

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1 ... CCTGCGCGGAGGGCCCTCGCACGGGCGCTCAATTCTATGACTGGCTGT 47
 451 CCTCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
 48 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 97
 501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
 98 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 147
 551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
 148 GATCAACGAAAACNCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 197
 601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650
 198 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 247
 651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700
 248 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 297
 701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
 298 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGANGAAACNGCTG 347
 751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
 348 TGGCCAAAGATCGGATCACANCCCTGT CANATCANTATCATGGCACNGCA 397
 801 TGGCCAAAGATCGGATCACAGCCCTGT CAGATCAGTATCATGGCACGGCA 850
 398 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 447
 851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
 448 ATTTAAANGAATCCATGGGCCA...ACCTCCCCCGTGATCCGGCGGTAA 493
 901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCTGATCGGGCGGTAA 950
 494 TGTGAC..... 499
 951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000

Fig. 5B

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360TNGCAGGTTGTGAGCA..TGCTACTTC 336
|:|||||||||||||
1101 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1150
335 GGTTTCAGGNGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 286
|||:|||||||||||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200
285 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 236
|||||||||||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGCAAACATGATCG 1250
235 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 186
|||||||||||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300
185 GACGTGCTGACCCCAGAGAAGATTNNTTCAAATGGCGACGATCGATGGGGC 136
|||||||||||||:|||||||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTCAAATGGCGACGATCGATGGGGC 1350
135 GCGTTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 86
|||:|||||||||
1351 GCG.TTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 1399
85 CGCGCGGACCTTATCCTGCTTGACCTGCGTCACCCTCAGACGACTCCTCA 36
|||||||||||||
1400 CGCGCGGACCTTATCCTGCTTGACCTGCGTCA..CCTCAGACGACTC..TC 1446
35 CCATCATTTGGCGGCCACGATCGTGTTTCAGGCTT..... 1
|||||||||
1447 ACATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGG 1496
.
.
.

Fig. 5C

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1 CGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 43
| | | | |
1451 CATTTGGCGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 1500
44 TGTCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 93
| | | | |
1501 TGTCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 1550
94 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 143
| | | | |
1551 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 1600
144 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 193
| | | | |
1601 ACAGCTATTTTGCACGCGGGCGAACATGGTGGCTAACCCAGCTTGGCGCA 1649
194 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 243
| | | | |
1650 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 1699
244 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 293
| | | | |
1700 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 1749
294 ATACAGAATTGCCATGAATGCGGCACTTCGTCCTTCGCTCGTGTGGAAT 343
| | | | |
1750 ATACAGAATTGCCATGAATGCGGCACTTCGTCCTTCGCTCGTGTGGAAT 1799
344 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 393
| | | | |
1800 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 1849
394 AGCCCGAGGATCCTCTAGAGTCCGATTTTCCGATGTCATCACCGGCGCG 443
| | | | |
1850 AGGCCCGAG 1858

Fig. 5D

105250 205500

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```

1    ... CCTGCGCGGA .GGCCTCCGCACGGGCGTCAATTCTATGACTGGCTGT 46
      |||||
451 CCTCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
      .
47   TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 96
      |||||
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
      .
97   GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 146
      |||||
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
      .
147  GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 196
      |||||
601  GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650
      .
197  CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 246
      |||||
651  CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700
      .
247  TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 296
      |||||
701  TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
      .
297  GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 346
      |||||
751  GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
      .
347  TGGCCAAAGATCGGATCACANCCCTGTCAGATCANTATCATGGCACGGCA 396
      |||||
801  TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850
      .
397  NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 446
      :|||
851  GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
      .
447  ATTTNAANGAATTCCATNGGCACAA .CCTTCCCCCGTGATCNGGCGGTAA 495
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
901  AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950
      .
496  TGTNGACCCA . . . . . 505
      ||| :|||
951  TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000

```

Fig. 6

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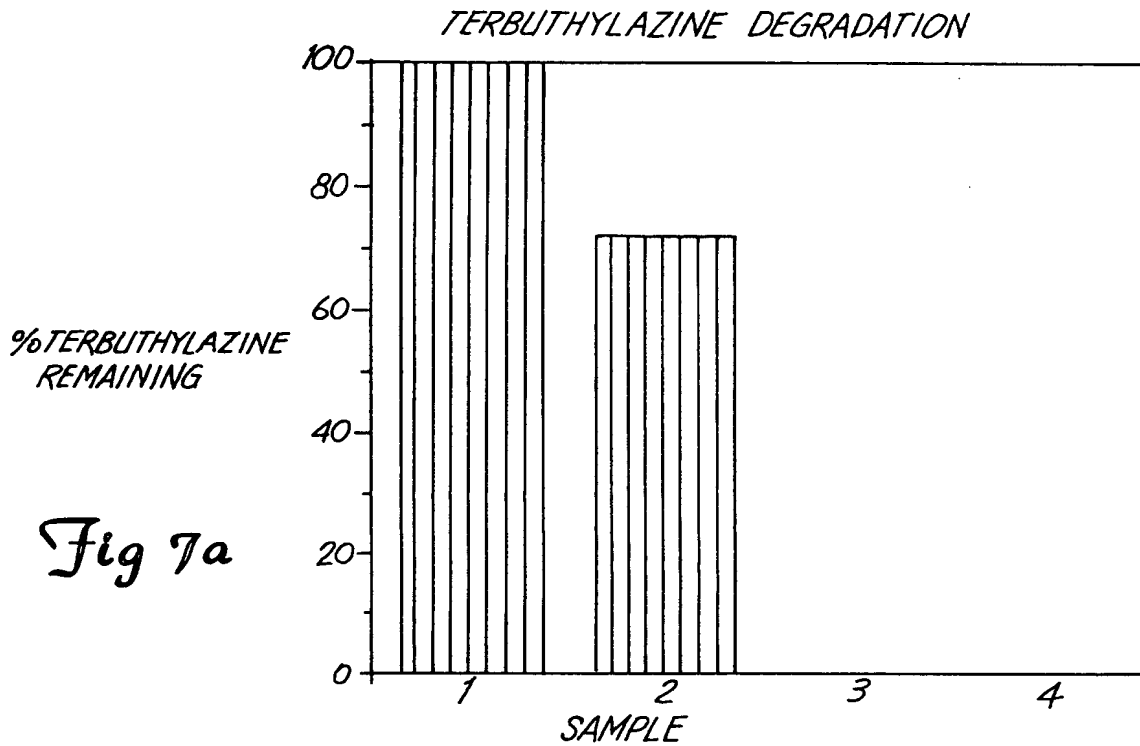


Fig 7a

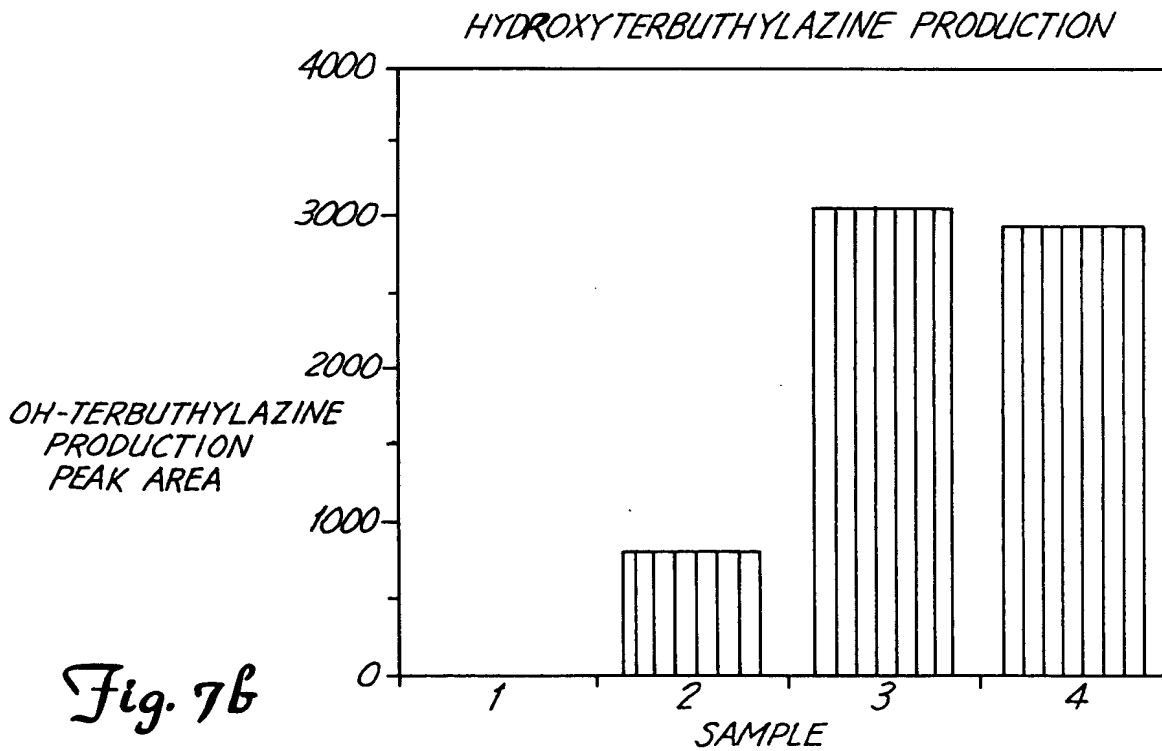


Fig. 7b

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TERBUTYLAZINE DEGRADATION BY SHUFFLED PROTEINS
 A7, A11 AND T7 - 1 μ g/ml ptn conc
 - EFFECT OF METAL IONS

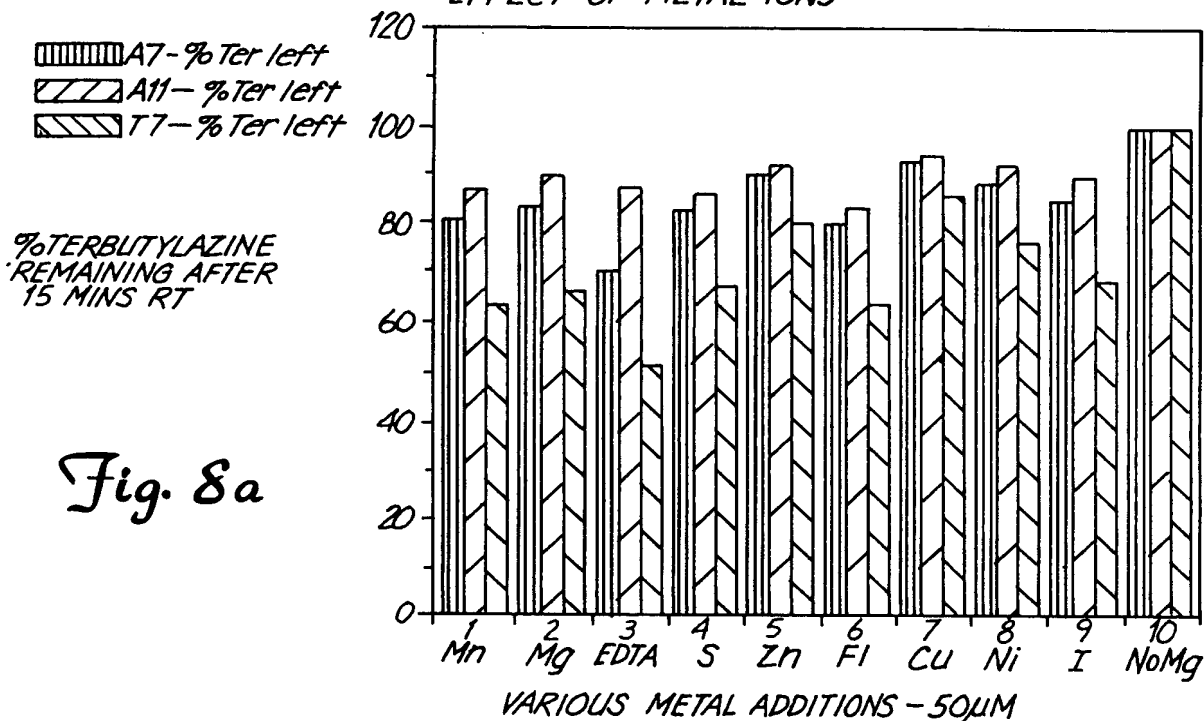
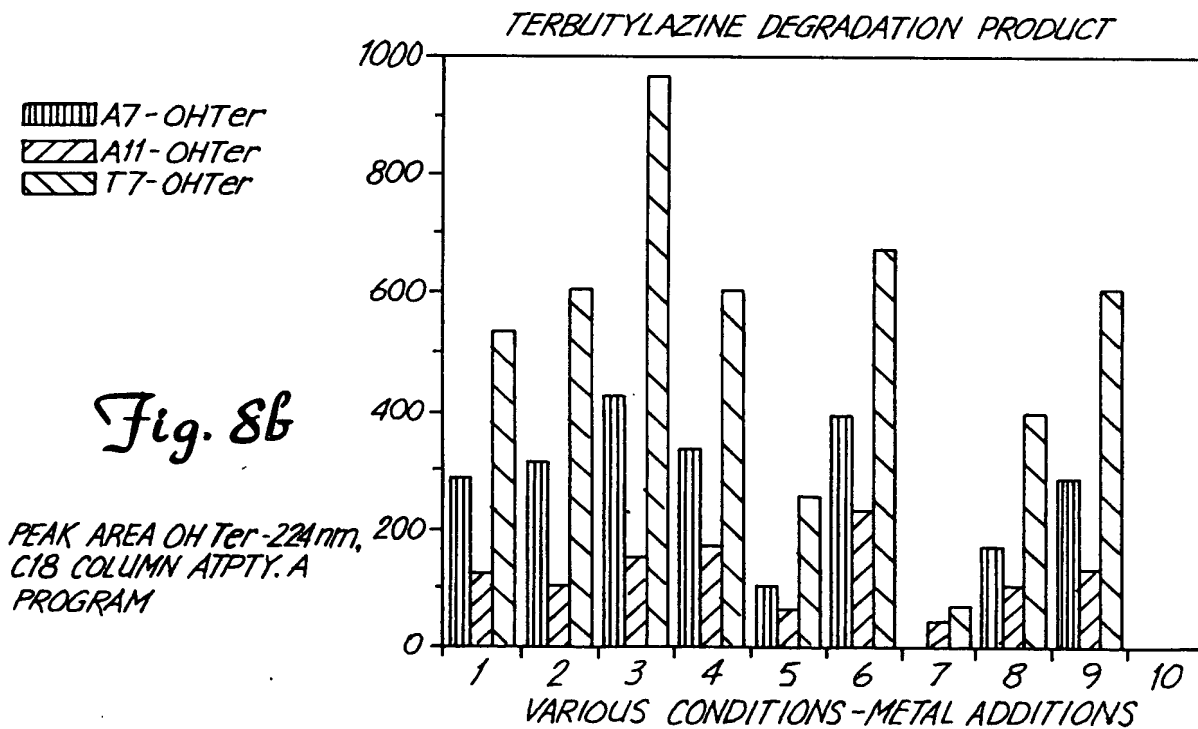


Fig. 8b



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Bacterium Translation of PCR amplified DNA sequence

		79	92		
ADP		SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
SG1		PHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
M91-3		SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
J14a		PHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
38/38		SHGRQ	FYDWLFNVLY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
Clav.		SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA EAVRSGITTI
		125			170
ADP	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
SG1	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
M91-3	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
J14a	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
38/38	NENNADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDTLK
Clav.	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
ADP	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
SG1	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
M91-3	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
J14a	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
38/38	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
CLav.	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT

Fig. 9